

## SEQUENCE LISTING

<110> DAICEL CHEMICAL INDUSTRIES, LTD.

<120> NOVEL ENONE REDUCTASES, METHODS FOR PRODUCING SAME, AND METHODS FOR SELECTIVELY REDUCING A CARBON-CARBON DOUBLE BOND OF AN  $\alpha, \beta$ -UNSATURATED KETONE USING THE REDUCTASES

<130> D1-A0103

<140>

<141>

<150> JP 2001-049363

<151> 2001-02-23

<160> 29

<170> PatentIn Ver. 2.1

<210> 1

<211> 1113

<212> DNA

<213> Kluyveromyces lactis

<220>

<221> CDS

<222> (1)..(1113)

<400> 1

atg tca gtt cca acc act caa aaa gcc gtc atc att gaa ggt gac aaa

Met Ser Val Pro Thr Thr Gln Lys Ala Val Ile Ile Glu Gly Asp Lys

1

5

10

15

48

gct gtt gtt aaa aca gat gtc tca gtt cca gaa tta aag gag ggt aca

Ala Val Val Lys Thr Asp Val Ser Val Pro Glu Leu Lys Glu Gly Thr

96

InS  
A2

1113

20	25	30	
gcc ttg gtg aag gtt gag gct gtt ggt aac cca act gat tgg aag			144
Ala Leu Val Lys Val Glu Ala Val Ala Gly Asn Pro Thr Asp Trp Lys			
35	40	45	
cat att gct tat aag att ggt cca gaa ggt tca att cta gga tgt gac			192
His Ile Ala Tyr Lys Ile Gly Pro Glu Gly Ser Ile Leu Gly Cys Asp			
50	55	60	
att gct ggt aca gtt gtc aaa ctt gga cca aat gct agt act gac ttg			240
Ile Ala Gly Thr Val Val Lys Leu Gly Pro Asn Ala Ser Thr Asp Leu			
65	70	75	80
aag gtt gga gat acc ggt ttc ggt ttt gtt cac ggt gct tcc caa aca			288
Lys Val Gly Asp Thr Gly Phe Gly Phe Val His Gly Ala Ser Gln Thr			
85	90	95	
gat cct aaa aat ggt gca ttt gct gaa tat gcc agg gtt tat cca cct			336
Asp Pro Lys Asn Gly Ala Phe Ala Glu Tyr Ala Arg Val Tyr Pro Pro			
100	105	110	
ttg ttt tac aag agt aac tta act cac tca act gct gat gaa att tct			384
Leu Phe Tyr Lys Ser Asn Leu Thr His Ser Thr Ala Asp Glu Ile Ser			
115	120	125	
gaa ggc cct gtg aag aac ttc gaa tct gct gca tca ttg cca gtt tcg			432
Glu Gly Pro Val Lys Asn Phe Glu Ser Ala Ala Ser Leu Pro Val Ser			
130	135	140	
ttg aca act gct ggt gtt agt ttg tgt cat cac ttg ggc tca aaa atg			480
Leu Thr Thr Ala Gly Val Ser Leu Cys His His Leu Gly Ser Lys Met			
145	150	155	160
gaa tgg cac cca tct acc ccg caa cat act cat cca tta ttg att tgg			528
Glu Trp His Pro Ser Thr Pro Gln His Thr His Pro Leu Leu Ile Trp			

165                    170                    175

ggt ggt gct aca gca gtg ggt caa caa cta atc caa gtt gcc aaa cat    576  
 Gly Gly Ala Thr Ala Val Gly Gln Gln Leu Ile Gln Val Ala Lys His  
 Gly Gly Ala Thr Ala Val Gly Gln Gln Leu Ile Gln Val Ala Lys His  
 180                    185                    190

atc aat gct tat act aag att gta act gtt gct tct aaa aag cat gaa    624  
 Ile Asn Ala Tyr Thr Lys Ile Val Thr Val Ala Ser Lys Lys His Glu  
 195                    200                    205

aag ctt tta aag tct tat ggt gct gat gat gtc ttt gac tat cat gat    672  
 Lys Leu Leu Lys Ser Tyr Gly Ala Asp Asp Val Phe Asp Tyr His Asp  
 210                    215                    220

gca ggc gtt att gag cag atc aac tcg aag tat cca aac ctg caa cat    720  
 Ala Gly Val Ile Glu Gln Ile Lys Ser Tyr Pro Asn Leu Gln His  
 225                    230                    235                    240

gtt att gac gct gtg gga agc gaa gat agt atc ccc gag gcc tat aaa    768  
 Val Ile Asp Ala Val Gly Ser Glu Asp Ser Ile Pro Glu Ala Tyr Lys  
 245                    250                    255

gtc aca gca gat agt cta cct gcc aca tta tta gaa gtg gtt cca atg    816  
 Val Thr Ala Asp Ser Leu Pro Ala Thr Leu Leu Glu Val Val Pro Met  
 260                    265                    270

acc att gaa agc att cct gaa gaa atc aga aaa gat aat gtt aaa att    864  
 Thr Ile Glu Ser Ile Pro Glu Glu Ile Arg Lys Asp Asn Val Lys Ile  
 275                    280                    285

gat att act ttg ttg tat cgt gca tct ggt caa gaa att cta ttg ggt    912  
 Asp Ile Thr Leu Leu Tyr Arg Ala Ser Gly Gln Glu Ile Leu Leu Gly  
 290                    295                    300

gca aca aga ttt cct gct agt cca gaa tat cat gaa gcc aca gtt aaa    960  
 Ala Thr Arg Phe Pro Ala Ser Pro Glu Tyr His Glu Ala Thr Val Lys

305

310

315

320

ttc gtt aag ttt ata aat cca cac ctt aac aac ggt gat atc cat cat 1008  
 Phe Val Lys Phe Ile Asn Pro His Leu Asn Asn Gly Asp Ile His His

325

330

335

atg aat att aaa gtt ttc agc aac ggc tta gat gat gtc cca gct ctc 1056  
 Met Asn Ile Lys Val Phe Ser Asn Gly Leu Asp Asp Val Pro Ala Leu

340

345

350

act gaa ggt ata aaa gaa ggt aaa aac aaa aat gtt aag tat gtt gcc 1104  
 Thr Glu Gly Ile Lys Glu Gly Lys Asn Lys Asn Val Lys Tyr Val Ala

355

360

365

agg tta taa 1113

Arg Leu

370

<210> 2

<211> 370

<212> PRT

<213> Kluyveromyces lactis

<400> 2

Met Ser Val Pro Thr Thr Gln Lys Ala Val Ile Ile Glu Gly Asp Lys

1

5

10

15

Ala Val Val Lys Thr Asp Val Ser Val Pro Glu Leu Lys Glu Gly Thr

20

25

30

Ala Leu Val Lys Val Glu Ala Val Ala Gly Asn Pro Thr Asp Trp Lys

35

40

45

His Ile Ala Tyr Lys Ile Gly Pro Glu Gly Ser Ile Leu Gly Cys Asp

50

55

60

Ile Ala Gly Thr Val Val Lys Leu Gly Pro Asn Ala Ser Thr Asp Leu

65

70

75

80

Lys Val Gly Asp Thr Gly Phe Phe Val His Gly Ala Ser Gln Thr

85	90	95
Asp Pro Lys Asn Gly Ala Phe Ala Glu Tyr Ala Arg Val Tyr Pro Pro		
100	105	110
Leu Phe Tyr Lys Ser Asn Leu Thr His Ser Thr Ala Asp Glu Ile Ser		
115	120	125
Glu Gly Pro Val Lys Asn Phe Glu Ser Ala Ala Ser Leu Pro Val Ser		
130	135	140
Leu Thr Thr Ala Gly Val Ser Leu Cys His His Leu Gly Ser Lys Met		
145	150	155
Glu Trp His Pro Ser Thr Pro Gln His Thr His Pro Leu Leu Ile Trp		
165	170	175
Gly Gly Ala Thr Ala Val Gly Gln Gln Leu Ile Gln Val Ala Lys His		
180	185	190
Ile Asn Ala Tyr Thr Lys Ile Val Thr Val Ala Ser Lys Lys His Glu		
195	200	205
Lys Leu Leu Lys Ser Tyr Gly Ala Asp Asp Val Phe Asp Tyr His Asp		
210	215	220
Ala Gly Val Ile Glu Gln Ile Lys Ser Lys Tyr Pro Asn Leu Gln His		
225	230	235
Val Ile Asp Ala Val Gly Ser Glu Asp Ser Ile Pro Glu Ala Tyr Lys		
245	250	255
Val Thr Ala Asp Ser Leu Pro Ala Thr Leu Leu Glu Val Val Pro Met		
260	265	270
Thr Ile Glu Ser Ile Pro Glu Glu Ile Arg Lys Asp Asn Val Lys Ile		
275	280	285
Asp Ile Thr Leu Leu Tyr Arg Ala Ser Gly Gln Glu Ile Leu Leu Gly		
290	295	300
Ala Thr Arg Phe Pro Ala Ser Pro Glu Tyr His Glu Ala Thr Val Lys		
305	310	315
Phe Val Lys Phe Ile Asn Pro His Leu Asn Asn Gly Asp Ile His His		
325	330	335
Met Asn Ile Lys Val Phe Ser Asn Gly Leu Asp Asp Val Pro Ala Leu		
340	345	350
Thr Glu Gly Ile Lys Glu Gly Lys Asn Asn Val Lys Tyr Val Ala		
355	360	365
Arg Leu		

370

&lt;210&gt; 3

&lt;211&gt; 1145

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (6).. (1136)

&lt;400&gt; 3

caaac atg tct gcc tcg att cca gaa acc atg aaa gcc gtt gtc att gaa 50

Met Ser Ala Ser Ile Pro Glu Thr Met Lys Ala Val Val Ile Glu

1

5

10

15

aat ggc aag gct gta gtc aaa cag gac att cca att cct gaa tta gaa 98

Asn Gly Lys Ala Val Val Lys Gln Asp Ile Pro Ile Pro Glu Leu Glu

20

25

30

gaa gga ttt gtt cta att aag act gtc gcc gtt gcc ggt aac cct acc 146

Glu Gly Phe Val Leu Ile Lys Thr Val Ala Val Ala Gly Asn Pro Thr

35

40

45

gat tgg aaa cat att gat ttc aag att ggt cct caa ggt gcc ctc tta 194

Asp Trp Lys His Ile Asp Phe Lys Ile Gly Pro Gln Gly Ala Leu Leu

50

55

60

ggc tgt gat gca gcc ggc caa atc gta aag ttg ggc cca aat gtt gat 242

Gly Cys Asp Ala Ala Gly Gln Ile Val Lys Leu Gly Pro Asn Val Asp

65

70

75

gct gca cgc ttt gcc att ggt gat tac att tat ggg gtt att cac ggt 290

Ala Ala Arg Phe Ala Ile Gly Asp Tyr Ile Tyr Gly Val Ile His Gly

80	85	90	95
<pre> gct tca gtg agg ttc ccc tca aac ggt gcc ttt gct gag tac tct gcc 338 Ala Ser Val Arg Phe Pro Ser Asn Gly Ala Phe Ala Glu Tyr Ser Ala           100           105           110 </pre>			
<pre> att tca tcc gag act gct tat aaa cca gcc aga gag ttt aga ttg tgc 386 Ile Ser Ser Glu Thr Ala Tyr Lys Pro Ala Arg Glu Phe Arg Leu Cys           115           120           125 </pre>			
<pre> ggt aaa gac aag cta cca gaa ggc ccc gta aaa tct tta gaa ggg gca 434 Gly Lys Asp Lys Leu Pro Glu Gly Pro Val Lys Ser Leu Glu Gly Ala           130           135           140 </pre>			
<pre> gta tcc ctc cca gtc tca ttg acc acg gct ggt atg atc ctt aca cat 482 Val Ser Leu Pro Val Ser Leu Thr Thr Ala Gly Met Ile Leu Thr His           145           150           155 </pre>			
<pre> agt ttt ggc ttg gac atg aca tgg aag ccc tcc aaa gcg caa aga gat 530 Ser Phe Gly Leu Asp Met Thr Trp Lys Pro Ser Lys Ala Gln Arg Asp           160           165           170           175 </pre>			
<pre> caa ccc atc tta ttt tgg ggt ggt gcc act gct gtt ggc cag atg ctt 578 Gln Pro Ile Leu Phe Trp Gly Ala Thr Ala Val Gly Gln Met Leu           180           185           190 </pre>			
<pre> att caa ttg gca aaa aaa cta aac ggt ttc agc aag atc atc gtc gtt 626 Ile Gln Leu Ala Lys Lys Leu Asn Gly Phe Ser Lys Ile Ile Val Val           195           200           205 </pre>			
<pre> gct tct cgt aaa cat gaa aaa ttg ttg aaa gag tac ggt gca gat gaa 674 Ala Ser Arg Lys His Glu Lys Leu Leu Lys Glu Tyr Gly Ala Asp Glu           210           215           220 </pre>			
<pre> ctt ttt gac tac cac gat gct gac gtt atc gaa cag ata aaa aag aag 722 Leu Phe Asp Tyr His Asp Ala Asp Val Ile Glu Gln Ile Lys Lys </pre>			

225

230

235

tac aac aac att cct tac ttg gtg gac tgt gtc tcc aac aca gaa act 770

Tyr Asn Asn Ile Pro Tyr Leu Val Asp Cys Val Ser Asn Thr Glu Thr

240

245

250

255

att caa cag gtg tac aaa tgt gcc gct gat gac tta gac gct acg gtc 818

Ile Gln Gln Val Tyr Lys Cys Ala Ala Asp Asp Leu Asp Ala Thr Val

260

265

270

gtt caa ttg acc gtt tta acc gaa aaa gat atc aag gag gaa gac agg 866

Val Gln Leu Thr Val Leu Thr Glu Lys Asp Ile Lys Glu Glu Asp Arg

275

280

285

agg caa aac gtc agt att gaa gga acc ctt cta tat ttg ata gga ggt 914

Arg Gln Asn Val Ser Ile Glu Gly Thr Leu Leu Tyr Leu Ile Gly Gly

290

295

300

aac gac gtc cca ttt ggc acg ttt act ttg cca gca gac cct gaa tac 962

Asn Asp Val Pro Phe Gly Thr Phe Thr Leu Pro Ala Asp Pro Glu Tyr

305

310

315

aag gaa gcc gcc ata aaa ttt att aag ttc atc aat cca aaa atc aat 1010

Lys Glu Ala Ala Ile Lys Phe Ile Lys Phe Ile Asn Pro Lys Ile Asn

320

325

330

335

gat ggt gaa atc cac cac atc cca gtg aaa gtt tac aag aac ggg tta 1058

Asp Gly Glu Ile His His Ile Pro Val Lys Val Tyr Lys Asn Gly Leu

340

345

350

gat gat atc cca cag tta ctt gat gat att aag cac ggg agg aat tct 1106

Asp Asp Ile Pro Gln Leu Leu Asp Asp Ile Lys His Gly Arg Asn Ser

355

360

365

ggc gaa aag ttg gtt gcc gtc ttg aaa taa tcttagactg 1145

Gly Glu Lys Leu Val Ala Val Leu Lys

370

375

&lt;210&gt; 4

&lt;211&gt; 376

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 4

Met Ser Ala Ser Ile Pro Glu Thr Met Lys Ala Val Val Ile Glu Asn  
 1                   5                   10                   15  
 Gly Lys Ala Val Val Lys Gln Asp Ile Pro Ile Pro Glu Leu Glu Glu  
 20                   25                   30  
 Gly Phe Val Leu Ile Lys Thr Val Ala Val Ala Gly Asn Pro Thr Asp  
 35                   40                   45  
 Trp Lys His Ile Asp Phe Lys Ile Gly Pro Gln Gly Ala Leu Leu Gly  
 50                   55                   60  
 Cys Asp Ala Ala Gly Gln Ile Val Lys Leu Gly Pro Asn Val Asp Ala  
 65                   70                   75                   80  
 Ala Arg Phe Ala Ile Gly Asp Tyr Ile Tyr Gly Val Ile His Gly Ala  
 85                   90                   95  
 Ser Val Arg Phe Pro Ser Asn Gly Ala Phe Ala Glu Tyr Ser Ala Ile  
 100                  105                  110  
 Ser Ser Glu Thr Ala Tyr Lys Pro Ala Arg Glu Phe Arg Leu Cys Gly  
 115                  120                  125  
 Lys Asp Lys Leu Pro Glu Gly Pro Val Lys Ser Leu Glu Gly Ala Val  
 130                  135                  140  
 Ser Leu Pro Val Ser Leu Thr Thr Ala Gly Met Ile Leu Thr His Ser  
 145                  150                  155                  160  
 Phe Gly Leu Asp Met Thr Trp Lys Pro Ser Lys Ala Gln Arg Asp Gln  
 165                  170                  175  
 Pro Ile Leu Phe Trp Gly Gly Ala Thr Ala Val Gly Gln Met Leu Ile  
 180                  185                  190  
 Gln Leu Ala Lys Lys Leu Asn Gly Phe Ser Lys Ile Ile Val Val Ala  
 195                  200                  205  
 Ser Arg Lys His Glu Lys Leu Leu Lys Glu Tyr Gly Ala Asp Glu Leu

210	215	220
Phe Asp Tyr His Asp Ala Asp Val Ile Glu Gln Ile Lys Lys Lys Tyr		
225	230	235
Asn Asn Ile Pro Tyr Leu Val Asp Cys Val Ser Asn Thr Glu Thr Ile		
245	250	255
Gln Gln Val Tyr Lys Cys Ala Ala Asp Asp Leu Asp Ala Thr Val Val		
260	265	270
Gln Leu Thr Val Leu Thr Glu Lys Asp Ile Lys Glu Glu Asp Arg Arg		
275	280	285
Gln Asn Val Ser Ile Glu Gly Thr Leu Leu Tyr Leu Ile Gly Gly Asn		
290	295	300
Asp Val Pro Phe Gly Thr Phe Thr Leu Pro Ala Asp Pro Glu Tyr Lys		
305	310	315
Glu Ala Ala Ile Lys Phe Ile Lys Phe Ile Asn Pro Lys Ile Asn Asp		
325	330	335
Gly Glu Ile His His Ile Pro Val Lys Val Tyr Lys Asn Gly Leu Asp		
340	345	350
Asp Ile Pro Gln Leu Leu Asp Asp Ile Lys His Gly Arg Asn Ser Gly		
355	360	365
Glu Lys Leu Val Ala Val Leu Lys		
370	375	

&lt;210&gt; 5

&lt;211&gt; 1134

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1134)

&lt;400&gt; 5

atg gct caa gtt gca att cca gaa acc atg aag gct gtc gtc att gaa 48  
 Met Ala Gln Val Ala Ile Pro Glu Thr Met Lys Ala Val Val Ile Glu

10

ac ggt aaa gcg gtt gtt aaa gag ggc att ccc att cct gaa ttg gaa	96
asp Gly Lys Ala Val Val Lys Glu Gly Ile Pro Ile Pro Glu Leu Glu	
20	25
gaa gga ttc gta ttg att aag aca ctc gct gtt ggt aac ccc act	144
Glu Gly Phe Val Leu Ile Lys Thr Leu Ala Val Ala Gly Asn Pro Thr	
35	40
gat tgg gca cac att gac tac aag atc ggg cct caa gga tct att ctg	192
Asp Trp Ala His Ile Asp Tyr Lys Ile Gly Pro Gln Gly Ser Ile Leu	
50	55
gga tgt gat gct ggc caa att gtc aaa ttg ggc cca gct gtc aat	240
Gly Cys Asp Ala Ala Gly Gln Ile Val Lys Leu Gly Pro Ala Val Asn	
65	70
cct aaa gac ttt tct atc ggt gat tat att tat ggg ttc att cac gga	288
Pro Lys Asp Phe Ser Ile Gly Asp Tyr Ile Tyr Gly Phe Ile His Gly	
85	90
tct tcc gta agg ttt cct tcc aat ggt gct ttt gct gaa tat tct gct	336
Ser Ser Val Arg Phe Pro Ser Asn Gly Ala Phe Ala Glu Tyr Ser Ala	
100	105
att tca act gtg gtt gcc tac aaa tca ccc aat gaa ctc aaa ttt ttg	384
Ile Ser Thr Val Val Ala Tyr Lys Ser Pro Asn Glu Leu Lys Phe Leu	
115	120
ggt gag gat gtt cta cct gcc ggc cct gtc agg tct ttg gaa ggt gta	432
Gly Glu Asp Val Leu Pro Ala Gly Pro Val Arg Ser Leu Glu Gly Val	
130	135
gcc act atc cca gtg tca ctg acc aca gcc ggc ttg gtg ttg acc tat	480
Ala Thr Ile Pro Val Ser Leu Thr Thr Ala Gly Leu Val Leu Thr Tyr	

145	150	155	160
aac ttg ggc ttg gac ctg aag tgg gag cca tca acc cca caa aga aaa 528			
Asn Leu Gly Leu Asp Leu Lys Trp Glu Pro Ser Thr Pro Gln Arg Lys			
165	170	175	
ggc ccc atc tta tta tgg ggc ggt gca act gca gta ggt cag tcg ctc 576			
Gly Pro Ile Leu Leu Trp Gly Ala Thr Ala Val Gly Gln Ser Leu			
180	185	190	
atc caa tta gcc aat aaa ttg aat ggc ttc acc aag atc att gtt gtg 624			
Ile Gln Leu Ala Asn Lys Leu Asn Gly Phe Thr Lys Ile Ile Val Val			
195	200	205	
gct tct cgg aag cac gaa aaa ctt ttg aaa gaa tat ggt gct gat gaa 672			
Ala Ser Arg Lys His Glu Lys Leu Leu Lys Glu Tyr Gly Ala Asp Glu			
210	215	220	
tta ttt gat tat cat gat att gac gtg gta gaa caa att aaa cac aag 720			
Leu Phe Asp Tyr His Asp Ile Asp Val Val Glu Gln Ile Lys His Lys			
225	230	235	240
tat aac aat atc tcg tat tta gtc gac tgt gtc gcg aat caa gat acg 768			
Tyr Asn Asn Ile Ser Tyr Leu Val Asp Cys Val Ala Asn Gln Asp Thr			
245	250	255	
ctt caa caa gtg tac aaa tgt gcg gcc gat aaa cag gat gct aca att 816			
Leu Gln Gln Val Tyr Lys Cys Ala Ala Asp Lys Gln Asp Ala Thr Ile			
260	265	270	
gtt gaa tta aaa aat ttg aca gaa gaa aac gtc aaa aaa gag aac agg 864			
Val Glu Leu Lys Asn Leu Thr Glu Glu Asn Val Lys Glu Asn Arg			
275	280	285	
aga caa aac gtt act att gac ata ata agg cta tat tca ata ggt ggc 912			
Arg Gln Asn Val Thr Ile Asp Ile Ile Arg Leu Tyr Ser Ile Gly Gly			

290

295

300

cat gaa gta cca ttt gga aac att act tta cca gcc gac tca gaa gct 960

His Glu Val Pro Phe Gly Asn Ile Thr Leu Pro Ala Asp Ser Glu Ala

305

310

315

320

agg aaa gct gca ata aaa ttt atc aaa ttc atc aat cca aag att aat 1008

Arg Lys Ala Ala Ile Lys Phe Ile Lys Phe Ile Asn Pro Lys Ile Asn

325

330

335

gat gga caa att cgc cat att cca gta agg gtc tat aag aac ggg ctt 1056

Asp Gly Gln Ile Arg His Ile Pro Val Arg Val Tyr Lys Asn Gly Leu

340

345

350

tgt gat gtt cct cat atc cta aaa gac atc aaa tat ggt aag aac tct 1104

Cys Asp Val Pro His Ile Leu Lys Asp Ile Lys Tyr Gly Lys Asn Ser

355

360

365

ggt gaa aaa ctc gtt gcc gta tta aac taa 1134

Gly Glu Lys Leu Val Ala Val Leu Asn

370

375

<210> 6

<211> 377

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 6

Met Ala Gln Val Ala Ile Pro Glu Thr Met Lys Ala Val Val Ile Glu

1

5

10

15

Asp Gly Lys Ala Val Val Lys Glu Gly Ile Pro Ile Pro Glu Leu Glu

20

25

30

Glu Gly Phe Val Leu Ile Lys Thr Leu Ala Val Ala Gly Asn Pro Thr

35

40

45

Asp Trp Ala His Ile Asp Tyr Lys Ile Gly Pro Gln Gly Ser Ile Leu

50	55	60
Gly Cys Asp Ala Ala Gly Gln Ile Val Lys Leu Gly Pro Ala Val Asn		
65	70	75
Pro Lys Asp Phe Ser Ile Gly Asp Tyr Ile Tyr Gly Phe Ile His Gly		80
85		90
Ser Ser Val Arg Phe Pro Ser Asn Gly Ala Phe Ala Glu Tyr Ser Ala		95
100	105	110
Ile Ser Thr Val Val Ala Tyr Lys Ser Pro Asn Glu Leu Lys Phe Leu		
115	120	125
Gly Glu Asp Val Leu Pro Ala Gly Pro Val Arg Ser Leu Glu Gly Val		
130	135	140
Ala Thr Ile Pro Val Ser Leu Thr Thr Ala Gly Leu Val Leu Thr Tyr		
145	150	155
Asn Leu Gly Leu Asp Leu Lys Trp Glu Pro Ser Thr Pro Gln Arg Lys		160
165		170
Gly Pro Ile Leu Leu Trp Gly Gly Ala Thr Ala Val Gly Gln Ser Leu		
180	185	190
Ile Gln Leu Ala Asn Lys Leu Asn Gly Phe Thr Lys Ile Ile Val Val		
195	200	205
Ala Ser Arg Lys His Glu Lys Leu Leu Lys Glu Tyr Ala Asp Glu		
210	215	220
Leu Phe Asp Tyr His Asp Ile Asp Val Val Glu Gln Ile Lys His Lys		
225	230	235
Tyr Asn Asn Ile Ser Tyr Leu Val Asp Cys Val Ala Asn Gln Asp Thr		240
245		250
Leu Gln Gln Val Tyr Lys Cys Ala Ala Asp Lys Gln Asp Ala Thr Ile		255
260	265	270
Val Glu Leu Lys Asn Leu Thr Glu Asn Val Lys Lys Glu Asn Arg		
275	280	285
Arg Gln Asn Val Thr Ile Asp Ile Ile Arg Leu Tyr Ser Ile Gly Gly		
290	295	300
His Glu Val Pro Phe Gly Asn Ile Thr Leu Pro Ala Asp Ser Glu Ala		
305	310	315
Arg Lys Ala Ala Ile Lys Phe Ile Lys Phe Ile Asn Pro Lys Ile Asn		320
325		330
Asp Gly Gln Ile Arg His Ile Pro Val Arg Val Tyr Lys Asn Gly Leu		335

340 345 350

Cys Asp Val Pro His Ile Leu Lys Asp Ile Lys Tyr Gly Lys Asn Ser

355 360 365

Gly Glu Lys Leu Val Ala Val Leu Asn

370 375

<210> 7

<211> 1122

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (7)..(1113)

<400> 7

gaaatc atg aaa gct gtc gtc att gaa gac ggt aaa gcg gtt gtc aaa 48

Met Lys Ala Val Val Ile Glu Asp Gly Lys Ala Val Val Lys

1 5 10

gag ggc gtt ccc att cct gaa ttg gaa gaa gga ttc gta ttg att aag 96

Glu Gly Val Pro Ile Pro Glu Leu Glu Gly Phe Val Leu Ile Lys

15 20 25 30

aca ctc gct gtt gct ggt aac ccg act gat tgg gca cac att gac tac 144

Thr Leu Ala Val Ala Gly Asn Pro Thr Asp Trp Ala His Ile Asp Tyr

35 40 45

aag gtc ggg cct caa gga tct att ctg gga tgt gac gct gcc ggc caa 192

Lys Val Gly Pro Gln Gly Ser Ile Leu Gly Cys Asp Ala Ala Gly Gln

50 55 60

att gtc aaa ttg ggc cca gcc gtc gat cct aaa gac ttt tct att ggt 240

Ile Val Lys Leu Gly Pro Ala Val Asp Pro Lys Asp Phe Ser Ile Gly

65

70

75

gat tat att tat ggg ttc att cac gga tct tcc gta agg ttt cct tcc 288  
 Asp Tyr Ile Tyr Gly Phe Ile His Gly Ser Ser Val Arg Phe Pro Ser

80

85

90

aat ggt gct ttt gct gaa tat tct gct att tca act gtg gtt gcc tac 336  
 Asn Gly Ala Phe Ala Glu Tyr Ser Ala Ile Ser Thr Val Val Ala Tyr  
 95 100 105 110

aaa tca ccc aat gaa ctc aaa ttt ttg ggt gaa gat gtt cta cct gcc 384  
 Lys Ser Pro Asn Glu Leu Lys Phe Leu Gly Glu Asp Val Leu Pro Ala  
 115 120 125

ggc cct gtc agg tct ttg gaa ggg gca gcc act atc cca gtg tca ctg 432  
 Gly Pro Val Arg Ser Leu Glu Gly Ala Ala Thr Ile Pro Val Ser Leu  
 130 135 140

acc aca gct ggc ttg gtg ttg acc tat aac ttg ggc ttg aac ctg aag 480  
 Thr Thr Ala Gly Leu Val Leu Thr Tyr Asn Leu Gly Leu Asn Leu Lys  
 145 150 155

tgg gag cca tca acc cca caa aga aac ggc ccc atc tta tta tgg ggc 528  
 Trp Glu Pro Ser Thr Pro Gln Arg Asn Gly Pro Ile Leu Leu Trp Gly  
 160 165 170

ggt gca act gca gta ggt cag tcg ctc atc caa tta gcc aat aaa ttg 576  
 Gly Ala Thr Ala Val Gly Gln Ser Leu Ile Gln Leu Ala Asn Lys Leu  
 175 180 185 190

aat ggc ttc acc aag atc att gtt gtg gct tct cgg aaa cac gaa aaa 624  
 Asn Gly Phe Thr Lys Ile Ile Val Val Ala Ser Arg Lys His Glu Lys  
 195 200 205

ctg ttg aaa gaa tat ggt gct gat caa cta ttt gat tac cat gat att 672  
 Leu Leu Lys Glu Tyr Gly Ala Asp Gln Leu Phe Asp Tyr His Asp Ile

210 215

220

gac gtg gta gaa caa att aaa cac aag tac aac aat atc tcg tat tta 720  
 Asp Val Val Glu Gln Ile Lys His Lys Tyr Asn Asn Ile Ser Tyr Leu

225 230

235

gtc gac tgt gtc gcg aat caa aat acg ctt caa caa gtg tac aaa tgt 768  
 Val Asp Cys Val Ala Asn Gln Asn Thr Leu Gln Gln Val Tyr Lys Cys

240 245

250

gct gcc gat aaa cag gat gct acc gtt gtc gaa tta act aat ttg aca 816  
 Ala Ala Asp Lys Gln Asp Ala Thr Val Val Glu Leu Thr Asn Leu Thr

255 260 265

270

gaa gaa aac gtc aaa aag gag aat agg agg caa aat gtc act att gac 864  
 Glu Glu Asn Val Lys Lys Glu Asn Arg Arg Gln Asn Val Thr Ile Asp

275 280 285

aga aca aga ctg tat tca ata ggc ggc cat gaa gta cca ttt ggt ggc 912  
 Arg Thr Arg Leu Tyr Ser Ile Gly Gly His Glu Val Pro Phe Gly Gly

290 295 300

att act ttc cct gct gac cca gaa gcc agg aga gct gcc acc gaa ttc 960  
 Ile Thr Phe Pro Ala Asp Pro Glu Ala Arg Arg Ala Ala Thr Glu Phe

305 310 315

gtc aag ttc atc aat cca aag att agt gat ggg caa att cac cat att 1008  
 Val Lys Phe Ile Asn Pro Lys Ile Ser Asp Gly Gln Ile His His Ile

320 325 330

cca gca agg gtc tat aag aac ggg ctt tac gat gtt cct cgt atc ctg 1056  
 Pro Ala Arg Val Tyr Lys Asn Gly Leu Tyr Asp Val Pro Arg Ile Leu

335 340 345 350

gaa gac att aaa atc ggt aag aac tct ggt gaa aaa ctc gtt gcc gta 1104  
 Glu Asp Ile Lys Ile Gly Lys Asn Ser Gly Glu Lys Leu Val Ala Val



Phe Thr Lys Ile Ile Val Val Ala Ser Arg Lys His Glu Lys Leu Leu  
 195 200 205  
 Lys Glu Tyr Gly Ala Asp Gln Leu Phe Asp Tyr His Asp Ile Asp Val  
 210 215 220  
 Val Glu Gln Ile Lys His Lys Tyr Asn Asn Ile Ser Tyr Leu Val Asp  
 225 230 235 240  
 Cys Val Ala Asn Gln Asn Thr Leu Gln Gln Val Tyr Lys Cys Ala Ala  
 245 250 255  
 Asp Lys Gln Asp Ala Thr Val Val Glu Leu Thr Asn Leu Thr Glu Glu  
 260 265 270  
 Asn Val Lys Lys Glu Asn Arg Arg Gln Asn Val Thr Ile Asp Arg Thr  
 275 280 285  
 Arg Leu Tyr Ser Ile Gly Gly His Glu Val Pro Phe Gly Gly Ile Thr  
 290 295 300  
 Phe Pro Ala Asp Pro Glu Ala Arg Arg Ala Ala Thr Glu Phe Val Lys  
 305 310 315 320  
 Phe Ile Asn Pro Lys Ile Ser Asp Gly Gln Ile His His Ile Pro Ala  
 325 330 335  
 Arg Val Tyr Lys Asn Gly Leu Tyr Asp Val Pro Arg Ile Leu Glu Asp  
 340 345 350  
 Ile Lys Ile Gly Lys Asn Ser Gly Glu Lys Leu Val Ala Val Leu Asn  
 355 360 365  
 365

<210> 9

<211> 12

<212> PRT

<213> Kluyveromyces lactis

<400> 9

Ser Tyr Gly Ala Asp Asp Val Phe Asp Tyr His Asp

1 5 10

<210> 10

<211> 12

<212> PRT

<213> Kluyveromyces lactis

<400> 10  
 Ile Gly Pro Glu Gly Ser Ile Leu Gly Cys Asp Ile  
     10  
     5  
     1

<210> 11

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:an artificially synthesized primer sequence

<220>

<221> misc\_feature

<222> (12)

<223> n indicates g, a, c or t.

<400> 11

tgrtartcra anacrtcrtc

20

<210> 12

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:an artificially synthesized primer sequence

<220>  
 <221> misc\_feature  
 <222> (18)  
 <223> n indicates g, a, c or t.

<400> 12  
 atwgggccwg argghtcnat

20

<210> 13  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:an artificially synthesized primer sequence

<220>  
 <221> misc\_feature  
 <222> (9)  
 <223> n indicates g, a, c or t.

<400> 13  
 atwggccng argghagyat

20

<210> 14  
 <211> 509  
 <212> DNA  
 <213> Kluyveromyces lactis

<400> 14  
 attggtccwg arggytcwat tctaggatgt gacattgctg gtacagtgt caaacttgga 60  
 ccaaattgcta gtactgactt gaaggttgga gataccgggt tcggtttgt tcacgggtc 120  
 tcccaaacag atcctaaaaa tggtgcattt gctgaatatg ccagggtta tccaccttg 180

ttttacaaga gtaactaac tcactcaact gctgatgaaa tttctgaagg ccctgtgaag 240  
 aacttcgaat ctgtcgcatc attgccagt tcgttgacaa ctgtggtgt tagtttgtt 300  
 catcaactgg gctcaaaaat ggaatggcac ccatctaccc cgcaacatac tcatccatta 360  
 ttgatttggg gtggtgctac agcagtgggt caacaactaa tccaagttgc caaacatatac 420  
 aatgcttata ctaagattgt aactgttgct tctaaaaagc atgaaaagct tttaaagtct 480  
 tatggtgctg atgacgtmmtt cgactacca 509

&lt;210&gt; 15

&lt;211&gt; 30

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:an artificially synthesized primer sequence

&lt;400&gt; 15

30

tccggtagcc acaactgtac cagcaatgtc

&lt;210&gt; 16

&lt;211&gt; 32

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:an artificially synthesized primer sequence

&lt;400&gt; 16

32

atcggtacct atactaagat tgtaactgtt gc

&lt;210&gt; 17

&lt;211&gt; 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:an artificially synthesized primer sequence

<400> 17

ccgggtaccc ttttagggtg a

21

<210> 18

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:an artificially synthesized primer sequence

<400> 18

tcatgaagcc acagttaat tcg

23

<210> 19

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:an artificially synthesized primer sequence

<400> 19

atattcatat gatggatatac accg

24

<210> 20

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:an artificially synthesized primer sequence

<400> 20

ctggaaattctt accatggctt cagttccaaac cactcaaaaa g

41

<210> 21

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:an artificially synthesized primer sequence

<400> 21

gacaaggcttc tagattataa cctggcaaca tacttaaca

39

<210> 22

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:an artificially synthesized primer sequence

25

<400> 22  
 caaacatgtc tgcctcgatt ccaga

<210> 23  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:an artificially  
 synthesized primer sequence

<400> 23  
 cagtctagat tatttcaaga cgccaaccaa c

31

<210> 24  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:an artificially  
 synthesized primer sequence

<400> 24  
 caaccatggc tcaaggta attccagaaa cc

32

<210> 25  
 <211> 38  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:an artificially synthesized primer sequence

<400> 25

gactctagat tagtttaata cggcaacgag ttttcac

38

<210> 26

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:an artificially synthesized primer sequence

<400> 26

gaaatcatga aagctgtcgt cattgaa

27

<210> 27

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:an artificially synthesized primer sequence

<400> 27

ttttcttagat tagtttaata cggcaackag tttttca

37

<210> 28

<211> 18

<212> DNA

*INS*

*SA*

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:an artificially synthesized primer sequence

<400> 28

tgtaaaaacga cggccagt

18

<210> 29

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:an artificially synthesized primer sequence

<400> 29

cagggaaacag ctatgacc

18